(1) GENERAL INFORMATION:

   (i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry; Van den Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

   (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof

   (iii) NUMBER OF SEQUENCES: 26

   (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Fulbright & Jaworski LLP
      (B) STREET: 666 Fifth Avenue
      (C) CITY: New York City
      (D) STATE: New York
      (F) ZIP: 10103

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
      (B) COMPUTER: IBM
      (C) OPERATING SYSTEM: PC-DOS
      (D) SOFTWARE: Wordperfect

   (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/819,669
      (B) FILING DATE: 17-March-1997
      (C) CLASSIFICATION: 435

   (vii) PRIOR APPLIATION DATA:
      (A) APPLICATION NUMBER: 08/142,368
      (B) FILING DATE: 02-MAY-1994

   (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: PCT/US92/04354
      (B) FILING DATE: 22-MAY-1992

   (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/807,043
      (B) FILING DATE: 12-DECEMBER-1991

   (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/764,364
      (B) FILING DATE: 23-SEPTEMBER-1991

   (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/728,838
      (b) FILING DATE: 9-JULY-1991

   (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/705,702

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(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Hanson, Norman D.
 (B) REGISTRATION NUMBER: 30,946
 (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (212)318-3168
 (B) TELEFAX: (212)752-5958

(2) INFORMATION FOR SEQUENCE ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 462 base pairs
  (B) TYPE: nucleic acid
  (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:


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ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT     120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG     180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC     240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT     300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT     360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT     420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                       462
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(2) INFORMATION FOR SEQUENCE ID NO: 2:
 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 675 base pairs
  (B) TYPE: nucleic acid
  (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:


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ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT      48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
                  5                  10                  15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA      96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
              20                  25                  30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA     144
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          Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
               35                      40                      45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG          192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
     50                      55                      60
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC          240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
 65                      70                      75                      80
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC          288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
                         85                      90                      95
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT          336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
                        100                     105                     110
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG          384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
                        115                     120                     125
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG          432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
                        130                     135                     140
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG          480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145                     150                     155                     160
AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC          528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
                        165                     170                     175
CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT          576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
                        180                     185                     190
GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG          624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
                        195                     200                     210
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT          672
Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
220                     225                     230                     235

TAG                                                                      675
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(2)   INFORMATION FOR SEQUENCE ID NO: 3:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 228 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:


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GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT          60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT         120
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TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC        180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                      228
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(2) INFORMATION FOR SEQUENCE ID NO: 4:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1365 base pairs
          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT   50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT   100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG   150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT   200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA   250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT   300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG   350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG   400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT   450
ACCCTTTGTG CC   462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA   504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG   546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC   588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC   630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC   672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG   714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC   756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT   798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA   840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA   882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT   924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT   966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG   1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT   1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG   1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT   1134
TAG   1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG   1187
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA   1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT   1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT   1337
GTTAAAAATA AAAGTTTGAC TTGCATAC   1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 4698 base pairs
          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

576670.1

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ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT      50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT     100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG     150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT     200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA     250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT     300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG     350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG     400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT     450
ACCCTTTGTG CC                                            462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA   504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG   546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC   588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC   630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC   672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG   714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC   756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT   798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA   840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA   882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T             916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA     966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC    1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC    1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC    1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC    1166
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC    1216
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC    1266
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT    1316
TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT    1366
TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT    1416
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG    1466
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT    1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT    1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC    1616
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG    1666
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG    1716
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT    1766
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT    1816
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC    1866
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT    1916
GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC    1966
AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT    2016
TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC    2066
CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT    2116
TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT    2166
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT    2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC    2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT    2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG    2366
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC    2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT    2466
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ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT      2516
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA      2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT      2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC      2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC      2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC      2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC      2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC      2866
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA      2916
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC      2966
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT      3016
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG      3066
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA      3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG      3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA      3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA      3266
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT      3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG                  3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT     3396
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT     3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA     3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA     3522
GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC     3564
TTC TCA CCT TAG                                             3576
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA      3626
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA      3676
TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA      3726
CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT      3776
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA      3826
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG      3876
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT      3926
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG      3976
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAGAG ATGAAAATCT       4026
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT      4076
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA      4126
AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA      4176
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA      4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC      4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC      4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT      4376
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA      4426
AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC      4476
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT      4526
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA      4576
TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT      4626
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA      4676
AATAAAAGTT TGACTTGCAT AC                                    4698
```

(2) INFORMATION FOR SEQUENCE ID NO: 6:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe
                5

(2) INFORMATION FOR SEQUENCE ID NO: 7:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2418 base pairs
          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG   50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC   100
TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG   150
GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT   200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT   250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA   300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT   350
CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC   400
TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC   450
CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG   500
TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT   550
CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT   600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC   650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG   700
GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC   750
CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC   800
AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA   850
CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG   900
TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT   950
TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG   1000
GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA   1050
GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG   1100
TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA   1150
GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC   1200
AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG   1250
CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT   1300
GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA   1350
TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC   1400
CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT   1450

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ATGTGAAAGT  CCTTGAGTAT  GTGATCAAGG  TCAGTGCAAG  AGTTCGCTTT       1500
TTCTTCCCAT  CCCTGCGTGA  AGCAGCTTTG  AGAGAGGAGG  AAGAGGGAGT       1550
CTGAGCATGA  GTTGCAGCCA  AGGCCAGTGG  GAGGGGGACT  GGGCCAGTGC       1600
ACCTTCCAGG  GCCGCGTCCA  GCAGCTTCCC  CTGCCTCGTG  TGACATGAGG       1650
CCCATTCTTC  ACTCTGAAGA  GAGCGGTCAG  TGTTCTCAGT  AGTAGGTTTC       1700
TGTTCTATTG  GGTGACTTGG  AGATTTATCT  TTGTTCTCTT  TTGGAATTGT       1750
TCAAATGTTT  TTTTTTAAGG  GATGGTTGAA  TGAACTTCAG  CATCCAAGTT       1800
TATGAATGAC  AGCAGTCACA  CAGTTCTGTG  TATATAGTTT  AAGGGTAAGA       1850
GTCTTGTGTT  TTATTCAGAT  TGGGAAATCC  ATTCTATTTT  GTGAATTGGG       1900
ATAATAACAG  CAGTGGAATA  AGTACTTAGA  AATGTGAAAA  ATGAGCAGTA       1950
AAATAGATGA  GATAAAGAAC  TAAAGAAATT  AAGAGATAGT  CAATTCTTGC       2000
CTTATACCTC  AGTCTATTCT  GTAAAATTTT  TAAAGATATA  TGCATACCTG       2050
GATTTCCTTG  GCTTCTTTGA  GAATGTAAGA  GAAATTAAAT  CTGAATAAAG       2100
AATTCTTCCT  GTTCACTGGC  TCTTTTCTTC  TCCATGCACT  GAGCATCTGC       2150
TTTTTGGAAG  GCCCTGGGTT  AGTAGTGGAG  ATGCTAAGGT  AAGCCAGACT       2200
CATACCCACC  CATAGGGTCG  TAGAGTCTAG  GAGCTGCAGT  CACGTAATCG       2250
AGGTGGCAAG  ATGTCCTCTA  AAGATGTAGG  GAAAAGTGAG  AGAGGGGTGA       2300
GGGTGTGGGG  CTCCGGGTGA  GAGTGGTGGA  GTGTCAATGC  CCTGAGCTGG       2350
GGCATTTTGG  GCTTTGGGAA  ACTGCAGTTC  CTTCTGGGGG  AGCTGATTGT       2400
AATGATCTTG  GGTGGATCC                                           2418


    (2)    INFORMATION FOR SEQUENCE ID NO: 8:
           (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH:  5724 base pairs
                (B)  TYPE:    nucleic acid
                (D)  TOPOLOGY:  linear
           (ii) MOLECULE TYPE:  genomic DNA
           (ix) FEATURE:
                (A)  NAME/KEY:  MAGE-1 gene
           (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 8:


CCCGGGGCAC  CACTGGCATC  CCTCCCCCTA  CCACCCCCAA  TCCCTCCCTT                50
TACGCCACCC  ATCCAAACAT  CTTCACGCTC  ACCCCAGCC   CAAGCCAGGC              100
AGAATCCGGT  TCCACCCCTG  CTCTCAACCC  AGGGAAGCCC  AGGTGCCCAG             150
ATGTGACGCC  ACTGACTTGA  GCATTAGTGG  TTAGAGAGAA  GCGAGGTTTT             200
CGGTCTGAGG  GGCGGCTTGA  GATCGGTGGA  GGGAAGCGGG  CCCAGCTCTG             250
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CCCCACATCC  CCCACCCCAT  CCCTCAACCC  TGATGCCCAT  CCGCCCAGCC             650
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CAGGCAGGAT  CCGGTTCCCG  CCAGGAAACA  TCCGGGTGCC  CGGATGTGAC             750
GCCACTGACT  TGCGCATTGT  GGGGCAGAGA  GAAGCGAGGT  TTCCATTCTG             800
AGGGACGGCG  TAGAGTTCGG  CCGAAGGAAC  CTGACCCAGG  CTCTGTGAGG             850
AGGCAAGGTG  AGAGGCTGAG  GGAGGACTGA  GGACCCCGCC  ACTCCAAATA             900


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(2) INFORMATION FOR SEQUENCE ID NO: 10:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 662 base pairs
          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY: MAGE-21 gene
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:


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(2) INFORMATION FOR SEQUENCE ID NO: 11:
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          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA to mRNA
     (ix) FEATURE:
          (A) NAME/KEY: cDNA MAGE-3
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:


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(2)   INFORMATION FOR SEQUENCE ID NO: 12:
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 943 base pairs
             (B) TYPE: nucleic acid
             (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (ix) FEATURE:
             (A) NAME/KEY: MAGE-31 gene
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC              790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT              832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC              874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG              916
GTG GCC AAG TTG GTT CAT TTT CTG CTC                                  943
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(2)    INFORMATION FOR SEQUENCE ID NO: 13:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH:  2531 base pairs
           (B) TYPE:    nucleic acid
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE:  genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY:  MAGE-4 gene
       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 13:
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GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG              50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC              100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG              150
GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT              200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT              250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA              300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT              350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA              400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC              450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT              500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC              550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG              600
CCTGCTGCCC TGACCAGAGT CATC                                          624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA              666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA              708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC              750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT              792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT              834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC              876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC              918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC              960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA              1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC              1044
ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA              1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG              1128
GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC              1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC              1212
```

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TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT                    1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG                    1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT                    1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG                    1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT                    1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT                    1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC                    1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA                    1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                                    1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC                     1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC                     1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT                     1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT                     1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT                     1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG                     1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG                     1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT                     1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA                     2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG                     2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA                     2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC                     2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA                     2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT                     2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT                     2328
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA                     2378
AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC                     2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC                     2478
TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT                     2528
GGG                                                                        2531
```

(2)   INFORMATION FOR SEQUENCE ID NO: 14:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2531 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (ix) FEATURE:
            (A) NAME/KEY: MAGE-41 gene
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:


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GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC                      100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG                      150
GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT                      200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT                      250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA                      300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT                      350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA                      400
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576670.1

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TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC          550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG          600
CCTGCTGCCC TGAGCAGAGT CATC                                      624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA         666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG         708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC         750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT         792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT         834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC         876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC         918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC         960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA         1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC         1044
ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA         1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG         1128
GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC         1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC         1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT         1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG         1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT         1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG         1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT         1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT         1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC         1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA         1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                         1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC          1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC          1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT          1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT          1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT          1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG          1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG          1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT          1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA          2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG          2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA          2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC          2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA          2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT          2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT          2328
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGCCTTTTG GGCTTTGGGA           2378
AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC          2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC          2478
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT          2528
GGG                                                            2531
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(2) INFORMATION FOR SEQUENCE ID NO: 15:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1068 base pairs
        (B) TYPE: nucleic acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA to mRNA
    (ix) FEATURE:
        (A) NAME/KEY: cDNA MAGE-4
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT         166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT         208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC         250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG         292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC         334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG         376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT         418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC         460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG         502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT         544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG         586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA         628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC         670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG          720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG          770
GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG          820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA          870
ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA          920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT          970
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT         1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC           1068
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(2) INFORMATION FOR SEQUENCE ID NO: 16:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2226 base pairs
        (B) TYPE: nucleic acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:
        (A) NAME/KEY: MAGE-5 gene
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG           50
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576670.1

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TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG          150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT          200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC          250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC          300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG          350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT          400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG          450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG          500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA          550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC          600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC               644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA         684
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG         728
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA         770
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA         812
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC         854
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG         896
TGG CTG ACT TGA                                                908
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA          958
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TCCTGAGAT          1008
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA          1058
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA          1108
CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG          1158
GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC          1208
CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG          1258
GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT          1308
TGGTGCAGGA AAACTACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC          1358
ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA          1408
CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC          1458
CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG          1508
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CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC          1608
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TGGATGACTT TGAGATTTGT CTTTGTTTCC TTTTGGAATT GTTCAAATGT          1708
TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA          1758
CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT          1808
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TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAAC          1908
TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC          1958
TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCTTGGC          2008
TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT          2058
TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC TGTGGAAGGC          2108
CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA          2158
CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT          2208
GCCCTCTAAG ATGTAGAG                                            2226
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GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG          50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC         100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG         150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT         200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC         250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC         300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG         350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT         400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG         450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG         500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA         550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC         600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC              644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA         686
GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC         728
AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT         770
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG         812
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA         854
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA         896
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC         938
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG         980
TGG CTG ACT TGA                                                992
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GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TCCTGAGAT         1092
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA        1142
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA        1192
CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC        1242
CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA        1292
GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG        1342
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CAGGAAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC        1442
TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG        1492
CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCTACC CATCCCTGCA         1542
TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG        1592
CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT        1642
CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCATT CTTCTCTCTT        1692
TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG        1742
ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCCTTT        1792
TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG        1842
TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA        1892
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TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC                    1942
AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAACTGATGA                    1992
GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC                    2042
GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT                    2092
TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT                    2142
GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG                    2192
GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG                    2242
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CTAAGATGTA GAG                                                           2305
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(2)   INFORMATION FOR SEQUENCE ID NO: 18:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 225 base pairs
              (B) TYPE: nucleic acid
              (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: cDNA
         (ix) FEATURE:
              (A) NAME/KEY: MAGE-6 gene
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG                     42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC                     84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC                    126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC                    168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC                    210
TGT GCC CCT GAG GAG                                                       225
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(2)   INFORMATION FOR SEQUENCE ID NO: 19:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1947 base pairs
              (B) TYPE: nucleic acid
              (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: genomic DNA
         (ix) FEATURE:
              (A) NAME/KEY: MAGE-7 gene
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA                     150
GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC                     200
ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT                     250
GGTTCACAAA TGAGGCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG                     300
GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA                     350
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GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG          450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA          500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA          550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA          600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC          650
TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA                          685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT         727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA         769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT         811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC         853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA         895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC         937
AGA GCA TGC CCG AGA CCG GCC TTC TGA                             964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG          1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT          1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC          1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT          1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG          1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG          1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC          1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC          1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT          1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG          1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC          1514
GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA AATGTTCCTT          1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG          1614
GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT          1664
TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG          1714
CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG          1764
GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG          1814
CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA          1864
GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA          1914
AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG                           1947
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(2)   INFORMATION FOR SEQUENCE ID NO: 20:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1810 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (ix) FEATURE:
            (A) NAME/KEY: MAGE-8 gene
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:


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GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA          50
TCACAGAGCA TAAGAGGCCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT          100
GTTTCCCCTG TATGTATACC AGAGGCCCCT CTGGCATCAG AACAGCAGGA          150
ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG          200
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GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA          250
GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA          300
CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA          350
CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT          400
CAATTGCCCA GCTCCGGCCC ACACTCTCCT GCTGCCCTGA CCTGAGTCAT          450
C                                                              451
ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA          493
GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG          535
CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC          577
TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT          619
GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT          661
TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT          703
GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC          745
CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT          787
GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA          829
TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG          871
AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC          913
AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT          955
GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC          997
ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT         1039
CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC         1081
ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC         1123
TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA                    1156
TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG         1206
AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT         1256
CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG         1306
CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA         1356
TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT         1406
TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG         1456
GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCCT GCTCTGTTAC         1506
ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA         1556
GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC         1606
AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG         1656
AATTGTTCCA ATGTTCCTTC TAATGGATGG TGTAATGAAC TTCAACATTC         1706
ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTTATA TAGTTTAGGA         1756
GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA         1806
ATTC                                                          1810
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(2)   INFORMATION FOR SEQUENCE ID NO: 21:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1412 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-9 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:


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TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC           50
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AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT          100
GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG          150
TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC          200
TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA          250
GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT          300
TGTTAGAACC TCCAAGGTTC GGTTCTCAGC TGAAGTCTCT CACACACTCC          350
CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC          400
CTGACTGCTG CCCTGACCAG AGTCATC                                  427
ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA          469
GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA          511
CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT          553
GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT          595
CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC          637
GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC          679
AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT          721
CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG          763
GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG          805
GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA          847
AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC          889
GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG          931
GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC          973
CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC          1015
AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC          1057
AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG          1099
AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC          1141
GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA          1183
AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG          1225
CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC          1267
AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA          1309
AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG          1351
GGA GAG GAG CAA GAG GGA GTC TGA                                1375
GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA                        1412
```

(2)   INFORMATION FOR SEQUENCE ID NO: 22:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 920 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-10 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:


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ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC ACCTACCCTA           50
CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT          100
CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA          150
AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT          200
GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA          250
CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC          300
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ACACTCCCAC CTGCTACCCT GATCAGAGTC ATC                          333
ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA        375
GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA        417
CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT        459
TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC        501
TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC        543
CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC        585
CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT        627
TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA        669
AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT        711
GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT        753
TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG        795
ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT        837
GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC        879
ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC         920


      (2)   INFORMATION FOR SEQUENCE ID NO: 23:
            (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH:  1107 base pairs
                  (B) TYPE:   nucleic acid
                  (D) TOPOLOGY:  linear
            (ii) MOLECULE TYPE:  genomic DNA
            (ix) FEATURE:
                  (A) NAME/KEY:  MAGE-11 gene
            (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 23:


AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT            50
CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT           100
CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG           150
GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG           200
AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG           250
CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC           300
AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC           350
ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC           400
TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC           450
TATCTGATGA GGGCTCTGGC AGCCAAGAAA GGAGGGGCC AAGTACCTCG            500
CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA           550
GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT           600
GATCACAAAG GCAGAA                                                616
ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT        658
GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT        700
GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT        742
GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG        784
TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA        826
GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA        868
GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT        910
GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT        952
ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG        994
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576670.1

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GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT          1036
CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG          1078
TAC ATA GCC AAT GCC AAT GGG AGG GAT CC                            1107
```

(2) INFORMATION FOR SEQUENCE ID NO: 24:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2150 base pairs
        (B) TYPE: nucleic acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:
        (A) NAME/KEY: smage-I
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:


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TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT           50
CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC          100
ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC          150
TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT          200
GCCCTTGTAT GCAGGCCTAA GTTTTTCTGT CTGCTTAACC CCTCCAAGTG          250
AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT          300
ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG          350
AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCCTAG AAAG               394
ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT          436
CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT          478
TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT          520
ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG          565
AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG          604
GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT          646
TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT          688
TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA          730
GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT          772
GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA          814
GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG          856
AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG          898
ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT          940
AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA          982
ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG         1024
GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA         1066
CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG         1108
TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC         1150
TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA         1192
TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG         1234
ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG         1276
GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC         1314
CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA         1360
ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT         1402
GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT         1444
CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA         1486
GGC AAG GGT GTT CAT CCA AGC GCC CCA TCC CAA AAG TCC TCT         1528
AAC ATG TAG                                                     1537
TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG          1587
AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCTGTTAT          1637
ACATTAGTAG AATGGAGGCT ATTTTTGTTA CTTTTCAAAT GTTTGTTTAA          1687
CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC          1737
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576670.1

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TGTCACTTGT CAGATTAGGA CTTGTTTTGT TATTTGCAAC AAACTGGAAA          1787
ACATTATTTT GTTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG          1837
GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG          1887
GGAAAGTTTA TATTGTTAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA          1937
TACTTTTTTC TTTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT          1987
GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAAACTC TATTACTTTA          2037
TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA          2087
GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA          2137
GTTATCAGAG TCT                                                  2150


    (2)    INFORMATION FOR SEQUENCE ID NO: 25:
           (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH:  2099 base pairs
                (B)  TYPE:    nucleic acid
                (D)  TOPOLOGY:  linear
           (ii) MOLECULE TYPE:  genomic DNA
           (ix) FEATURE:
                (A)  NAME/KEY:  smage-II
           (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 25:


ACCTTATTGG GTCTGTCTGC ATATGCCTCC ACTTGTGTGT AGCAGTCTCA            50
AATGGATCTC TCTCTACAGA CCTCTGTCTG TGTCTGGCAC CCTAAGTGGC           100
TTTGCATGGG CACAGGTTTC TGCCCCTGCA TGGAGCTTAA ATAGATCTTT           150
CTCCACAGGC CTATACCCCT GCATTGTAAG TTTAAGTGGC TTTATGTGGA           200
TACAGGTCTC TGCCCTTGTA TGCAGGCCTA AGTTTTTCTG TCTGCTTAGC           250
CCCTCCAAGT GAAGCTAGTG AAAGATCTAA CCCACTTTTG GAAGTCTGAA           300
ACTAGACTTT TATGCAGTGG CCTAACAAGT TTTAATTTCT TCCACAGGGT           350
TTGCAGAAAA GAGCTTGATC CACGAGTTCG GAAGTCCTGG TATGTTCCTA           400
GAAAGATGTT CTCCTGGAAA GCTTCAAAAG CCAGGTCTCC ATTAAGTCCA           450
AGGTATTCTC TACCTGGTAG TACAGAGGTA CTTACAGGTT GTCATTCTTA           500
TCTTTCCAGA TTCCTGTCTG CCAGCTCTTT TACTTCAGCC CTGAGCACAG           550
TCAACATGCC TAGGGGTCAA AAGAGTAAGA CCCGCTCCCG TGCAAAACGA           600
CAGCAGTCAC GCAGGGAGGT TCCAGTAGTT CAGCCCACTG CAGAGGAAGC           650
AGGGTCTTCT CCTGTTGACC AGAGTGCTGG GTCCAGCTTC CCTGGTGGTT           700
CTGCTCCTCA GGGTGTGAAA ACCCCTGGAT CTTTTGGTGC AGGTGTATCC           750
TGCACAGGCT CTGGTATAGG TGGTAGAAAT GCTGCTGTCC TGCCTGATAC           800
AAAAAGTTCA GATGGCACCC AGGCAGGGAC TTCCATTCAG CACACACTGA           850
AAGATCCTAT CATGAGGAAG GCTAGTGTGC TGATAGAATT CCTGCTAGAT           900
AAGTTTAAGA TGAAAGAAGC AGTTACAAGG AGTGAAATGC TGGCAGTAGT           950
TAACAAGAAG TATAAGGAGC AATTCCCTGA GATCCTCAGG AGAACTTCTG          1000
CACGCCTAGA ATTAGTCTTT GGTCTTGAGT TGAAGGAAAT TGATCCCAGC          1050
ACTCATTCCT ATTTGCTGGT AGGCAAACTG GGTCTTTCCA CTGAGGGAAG          1100
TTTGAGTAGT AACTGGGGGT TGCCTAGGAC AGGTCTCCTA ATGTCTGTCC          1150
TAGGTGTGAT CTTCATGAAG GGTAACCGTG CCACTGAGCA AGAGGTCTGG          1200
CAATTTCTGC ATGGAGTGGG GGTATATGCT GGGAAGAAGC ACTTGATCTT          1250
TGGCGAGCCT GAGGAGTTTA TAAGAGATGT AGTGCGGGAA AATTACCTGG          1300
AGTACCGCCA GGTACCTGGC AGTGATCCCC CAAGCTATGA GTTCCTGTGG          1350
GGACCCAGAG CCCATGCTGA AACAACCAAG ATGAAAGTCC TGGAAGTTTT          1400
AGCTAAAGTC AATGGCACAG TCCCTAGTGC CTTCCCTAAT CTCTACCAGT          1450
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TGGCTCTTAG AGATCAGGCA GGAGGGGTGC CAAGAAGGAG AGTTCAAGGC           1500
AAGGGTGTTC ATTCCAAGGC CCCATCCCAA AAGTCCTCTA ACATGTAGTT           1550
GAGTCTGTTC TGTTGTGTTT GAAAAACAGT CAGGCTCCTA ATCAGTAGAG           1600
AGTTCATAGC CTACCAGAAC CAACATGCAT CCATTCTTGG CCTGTTATAC           1650
ATTAGTAGAA TGGAGGCTAT TTTTGTTACT TTTCAAATGT TTGTTTAACT           1700
AAACAGTGCT TTTTGCCATG CTTCTTGTTA ACTGCATAAA GAGGTAACTG           1750
TCACTTGTCA GATTAGGACT TGTTTTGTTA TTTGCAACAA ACTGGAAAAC           1800
ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA           1850
TTGTCATGGC AATGTGATAT CATACAGTGG TGAAACAACA GTGAAGTGGG           1900
AAAGTTTATA TTGTTAGTTT TGAAAATTTT ATGAGTGTGA TTGCTGTATA           1950
CTTTTTTCTT TTTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA           2000
CTTTACTCAA ATTCATTAGA AAGTAAATCA TAAAACTCTA TTACTTTATT           2050
ATTTTCTTCA ATTATTAATT AAGCATTGGT TATCTGGAAG TTTCTCCAG            2099
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(2)   INFORMATION FOR SEQUENCE ID NO: 26:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 9 amino acids
           (B) TYPE: amino acids
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
                5